IN THE CLAIMS:

Provided below is a clean copy of all claims.

1. (Amended) A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous probes, wherein at least one of the two homologous probes is a non-linear probe, said method comprising:

introducing a mismatch with an intended target sequence in said non-linear probe; and

conducting a hybridization reaction using said at least two homologous probes, thereby reducing the background signals of the hybridization reaction.

2. (Amended) A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous target sequences, said method comprising:

providing for an intended mismatch between at least one of the two homologous target sequences and at least one non-linear probe; and

conducting a hybridization reaction using said at least two homologous target sequences, thereby reducing the background signals of the hybridization reaction.

3. (Amended) The method according to claim 1 in which the homologous probes are designed to detect point mutations in at least one target sequence.

4. The method according to claim 2, wherein at least two of said non-linear probes and/or two of said target sequences comprise an identical sequence except for a variation due to a point mutation or due to a mismatch in a nucleotide sequence.

5. (Amended) The method according to claim 1, wherein the mismatch in a nucleotide sequence comprises 1-3 nucleotides.

6. (Amended) The method according to claim 2, wherein the mismatch in a nucleotide sequence is located between 2 and 20 nucleotides upstream or downstream of a point mutation.

7. (Amended) The method according to claim 1 wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

8. (Amended) The method according to claim 1 wherein the at least one of the non-linear probes is provided with a detectable moiety.

9. (Amended) The method according to claim 1, further comprising amplifying a nucleic acid sequence.

16. (Amended) A method of conducting a hybridization reaction comprising:

mixing a set of homologous probes for detecting at least one allelic variant of a nucleic acid, wherein at least one of said set of homologous probes is non-linear, said set of homologous probes comprising at least one sequence completely complementary to and specific for one of the allelic variants of said nucleic acid, except for a specific mismatch located upstream, downstream or both upstream and downstream from the site of variation;

detecting variants of the nucleic acids; and

using the set of homologous probes to conduct the hybridization reaction.

17. The method according to claim 16 wherein the nucleic acids are derived from a group of pathogens.

18. The method according to claim 17 wherein the nucleic acids represent a number of HIV-variants.

21. The method according to claim 2 in which the homologous probes are designed to detect point mutations in at least one target sequence.

22. The method according to claim 2, wherein the mismatch in a nucleotide sequence comprises 1-3 nucleotides.

23. The method according to claim 2 wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

24. The method according to claim 2 wherein the at least one of the non-linear probes is provided with a detectable moiety.

25. The method according to claim 2, further comprising amplifying a nucleic acid sequence.